

gibberellin signals are integrated to *AGL20*. We suggest that *AGL20* protein integrates signals from different pathways of floral induction including the gibberellin pathway which is crucial in short day conditions and is a central component for the induction of flowering in *Arabidopsis*.

F207 Arabidopsis Cytochrome P450 Mutants Involved in Maintaining Apical Dominance and Fruit Elongation

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Cytochrome P450s are involved in the metabolism of most phytohormones as well as many secondary metabolites in plant cells. Sequencing of the *Arabidopsis* genome revealed that it contains six different CYP78A genes, CYP78A5 to 78A10. In an effort to elucidate the functional roles of CYP78A genes in *A. thaliana*, we isolated knock-out mutants for these genes by reverse genetics method. Only *cyp78A5* mutant showed a visible phenotype having slightly reduced apical dominance. To further elucidate function and to circumvent gene redundancy, we generated double mutant lines based on gene expression patterns (*cyp78A5/78A7*) and sequence identity (*cyp78A6/78A9*). A double mutant, *cyp78A5/78A7*, showed pleiotropic phenotypes: dwarfism, sterility, multiple inflorescences, short hypocotyls, and delayed senescence. The double mutant also displayed very abnormal inflorescence growth pattern where flower inflorescence progressively arose out of disorganized clusters of cauline leaves. Transgenic lines overexpressing CYP78A7 showed strong apical dominance and defects in floral development. The other double mutant, *cyp78A6/78A9*, shows short silique phenotype. The silique length of *cyp78A6/*

78A9 double mutant reduced by 40% compared to wild-type, and single mutants, *cyp78A6* and *cyp78A9*, but the seed number and the seed size were not changed. We will discuss the putative functional roles of the CYP78A genes in growth and development of *Arabidopsis*.

F301 PCR Cloning of *mmoZ* Gene Encoding a Hydroxylase of Soluble Methane Monooxygenase from *Methylocystis* sp. strain 2

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Several methanotrophs synthesize a soluble cytoplasmic methane monooxygenase (sMMO) when they are grown in copper-depleted conditions. A 348 bp fragment of the *mmoZ* gene encoding the binding protein of soluble methane monooxygenase was cloned by polymerase chain reaction (PCR) and sequenced from *Methylocystis* sp. strain 2. The cloned gene had approximately 91.6% homology with other *mmoZ* genes in nucleotide sequence level. The deduced amino acid sequence showed about 46% homology with those from other methanotrophic and methylotrophic bacteria and several key amino acids were also found. These results suggest that this strain has the same methane-oxidizing system as in other methanotrophic bacteria.

F302 Purification and Characterization of Methanol Dehydrogenase (MDH) from a Marine Methylotroph *Methylophaga* sp. strain YC

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Methanol dehydrogenase (MDH) was purified from a marine methylotroph *Methylophaga* sp. strain YC using ammonium sulfate fractionation, anion-exchange chromatography, and gel permeation chromatography in order. The relative molecular mass of the native enzyme was found to be 145 kDa. The purified MDH was composed of two subunits having 64 kDa and 12 kDa in size, as judged by SDS-PAGE. These results suggest that the MDH from *Methylophaga* sp. strain YC is composed of two subunits with an 22 conformation as in other MDHs. Interestingly, the purified enzyme could maintain its activity even in high alkali and the optimum activity could be observed at 60?, not at 30?. The estimated Km values were 0.93 mM for methanol and 2.16 mM for ethanol, respectively when they were used as substrates. The enzymatic activity of the purified MDH was strongly inhibited by Fe²⁺ ion, not by EDTA.

F601 Genetic Variation of Apolipoprotein AI-CIII Gene Cluster in Korean Essential Hypertensives

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Essential Hypertension is a multifactorial disease associated with lipid metabolism. The apolipoprotein AI and CIII (apo AI and CIII) are known to play an important role

in the metabolism of plasma lipoproteins and lipids. The apo AI-CIII gene cluster is located in chromosome 11q23 and more than 20 different RFLPs have been described in this gene cluster. To search for a useful genetic marker on the essential hypertension in Korean population, we investigated the distribution of alleles of Msp I polymorphism located in the APO AI gene and a Sst I polymorphism located in the APO CIII gene in 163 Korean individuals. The allele or genotype frequency Sst I RFLP at the APO CIII gene was not significantly different between the two groups- normotensive and hypertensive. However, the Msp I RFLP of the apo AI gene was significantly ($P < 0.05$) associated with essential hypertension in Korean population. The distribution of the genotypes of all RFLPs was in Hardy-Weinberg equilibrium in this population. Therefore, this result suggest that this polymorphism of the apo AI gene may be useful as a genetic marker on the essential hypertension in Korean population.

F801 Role of Xanthine Dehydrogenase and Aging on the Innate Immune Response of Drosophila

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It has been proposed that uric acid is an important scavenger of deleterious oxygen species and peroxynitrite in biological systems. The cellular sources responsible for the generation of damage-causing reactive oxygen species (ROS) are widespread. It has been proposed that uric acid is an important scavenger of deleterious oxygen species and peroxynitrite